

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Fuerst, Thomas R.  
McAtee, C. Patrick  
Yarbough, Patrice O.  
Zhang, Yifan
- 10 (ii) TITLE OF INVENTION: HEPATITIS E VIRUS ANTIGENS AND USES THEREFOR
- (iii) NUMBER OF SEQUENCES: 31
- (iv) CORRESPONDENCE ADDRESS:
- 15 (A) ADDRESSEE: Dehlinger & Associates  
(B) STREET: 350 Cambridge Ave., Suite 250  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: USA  
20 (F) ZIP: 94306
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:  
30 (B) FILING DATE:  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Fabian, Gary R.  
35 (B) REGISTRATION NUMBER: 33,875  
(C) REFERENCE/DOCKET NUMBER: 4600-0293.30
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (415) 324-0880  
40 (B) TELEFAX: (415) 324-0960

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 2049 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

10

## (iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

- 15 (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain)  
ORF-2

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

20 ATGCGCCCTC GGCCTATTTT GTTGCTGCTC CTCATGTTTT TGCCTATGCT GCCCGCGCCA 60  
CCGCCCCGGTC AGCCGTCTGG CCGCCGTCGT GGGCGGCGCA GCGGCGGTTC CGGCGGTGGT 120  
TTCTGGGGTG ACCGGGTGA TTCTCAGCCC TTCGCAATCC CCTATATTCA TCCAACCAAC 180  
25 CCCTTCGCCC CCGATGTCAC CGCTGCGGCC GGGGCTGGAC CTCGTGTTTC CCAACCCGCC 240  
CGACCACTCG GCTCCGCTTG GCGTGACCAG GCCCAGCGCC CCGCCGTTGC CTCACGTCGT 300  
30 AGACCTACCA CAGCTGGGGC CGCGCCGCTA ACCGCGGTTC CTCCGGCCCA TGACACCCCG 360  
CCAGTGCCTG ATGTCGACTC CCGCGGCGCC ATCTTGCGCC GGCAGTATAA CCTATCAACA 420  
TCTCCCCTTA CCTCTCCGT GGCCACCGGC ACTAACCTGG TTCTTTATGC CGCCCCTCTT 480  
35 AGTCCGCTTT TACCCCTTCA GGACGGCACC AATACCCATA TAATGGCCAC GGAAGCTTCT 540  
AATTATGCCC AGTACCGGGT TGCCCGTGCC ACAATCCGTT ACCGCCCCGCT GGTCCCCAAT 600  
40 GCTGTCGGCG GTTACGCCAT CTCCATCTCA TTCTGGCCAC AGACCACCAC CACCCCGACG 660

	TCCGTTGATA	TGAATTCAAT	AACCTCGACG	GATGTTTCGT	TTTTAGTCCA	GCCCCGGCATA	720
	GCCTCTGAGC	TTGTGATCCC	AAGTGAGCGC	CTACACTATC	GTAACCAAGG	CTGGCGCTCC	780
5	GTCGAGACCT	CTGGGGTGGC	TGAGGAGGAG	GCTACCTCTG	GTCTTGTTAT	GCTTTGCATA	840
	CATGGCTCAC	TCGTAAATTC	CTATACTAAT	ACACCCTATA	CCGGTGCCCT	CGGGCTGTTG	900
	GACTTTGCCC	TTGAGCTTGA	GTTTCGCAAC	CTTACCCCCG	GTAACACCAA	TACGCGGGTC	960
10	TCCCGTTATT	CCAGCACTGC	TCGCCACCGC	CTTCGTCGCG	GTGCGGACGG	GA CTGCCGAG	1020
	CTCACCACCA	CGGCTGCTAC	CCGCTTTATG	AAGGACCTCT	ATTTTACTAG	TACTAATGGT	1080
15	GTCGGTGAGA	TCGGCCGCGG	GATAGCCCTC	ACCCTGTTCA	ACCTTGCTGA	CACTCTGCTT	1140
	GGCGGCCTGC	CGACAGAATT	GATTTTCGTCG	GCTGGTGGCC	AGCTGTTCTA	CTCCCGTCCC	1200
	GTTGTCTCAG	CCAATGGCGA	GCCGACTGTT	AAGTTGTATA	CATCTGTAGA	GAATGCTCAG	1260
20	CAGGATAAGG	GTATTGCAAT	CCCGCATGAC	ATTGACCTCG	GAGAATCTCG	TGTGGTTATT	1320
	CAGGATTATG	ATAACCAACA	TGAACAAGAT	CGGCCGACGC	CTTCTCCAGC	CCCATCGCGC	1380
25	CCTTTCTCTG	TCCTTCGAGC	TAATGATGTG	CTTTGGCTCT	CTCTCACC GC	TGCCGAGTAT	1440
	GACCAGTCCA	CTTATGGCTC	TTCGACTGGC	CCAGTTTATG	TTTCTGACTC	TGTGACCTTG	1500
	GTTAATGTTG	CGACCGGCGC	GCAGGCCGTT	GCCCCGGTCGC	TCGATTGGAC	CAAGGTCACA	1560
30	CTTGACGGTC	GCCCCCTCTC	CACCATCCAG	CAGTACTCGA	AGACCTTCTT	TGTCCTGCCG	1620
	CTCCGCGGTA	AGCTCTCTTT	CTGGGAGGCA	GGCACA ACTA	AAGCCGGGTA	CCCTTATAAT	1680
35	TATAACACCA	CTGCTAGCGA	CCAACTGCTT	GTCGAGAATG	CCGCCGGGCA	CCGGGTCGCT	1740
	ATTTCCACTT	ACACCACTAG	CCTGGGTGCT	GGTCCCGTCT	CCATTTCTGC	GGTTGCCGTT	1800
	TTAGCCCCCC	ACTCTGCGCT	AGCATTGCTT	GAGGATACCT	TGGACTACCC	TGCCCCGCGC	1860
40	CATACTTTTG	ATGATTTCTG	CCCAGAGTGC	CGCCCCCTTG	GCCTTCAGGG	CTGCGCTTTC	1920

CAGTCTACTG TCGCTGAGCT TCAGCGCCTT AAGATGAAGG TGGGTAAAAC TCGGGAGTTG 1980  
 TAGTTTATTT GCTTGTGCCC CCCTTCTTTC TGTGCTTAT TTCTCATTTT TCGGTTCCGC 2040  
 5 GCTCCCTGA 2049

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 2058 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

20 (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico Strain)  
 ORF-2 region

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

25 ATGCGCCCTA GGCCTCTTTT GCTGTTGTTT CTCTTGTTTC TGCCTATGTT GCCCGCGCCA 60  
 CCGACCGGTC AGCCGTCTGG CCGCCGTCGT GGGCGGCGCA GCGGCGGTAC CGGCGGTGGT 120  
 TTCTGGGGTG ACCGGGTTGA TTCTCAGCCC TTCGCAATCC CCTATATTCA TCCAACCAAC 180  
 30 CCCTTTGCCC CAGACGTTGC CGCTGCGTCC GGGTCTGGAC CTCGCCTTCG CCAACCAGCC 240  
 CGGCCACTTG GCTCCACTTG GCGAGATCAG GCCCAGCGCC CCTCCGCTGC CTCCCGTCGC 300  
 35 CGACCTGCCA CAGCCGGGGC TCGGCGCTG ACGGCTGTGG CGCCTGCCCA TGACACCTCA 360  
 CCCGTCCCGG ACGTTGATTC TCGCGGTGCA ATTCTACGCC GCCAGTATAA TTTGTCTACT 420  
 TCACCCCTGA CATCCTCTGT GGCCTCTGGC ACTAATTTAG TCCTGTATGC AGCCCCCTT 480  
 40 AATCCGCCTC TGCCGCTGCA GGACGGTACT AATACTCACA TTATGGCCAC AGAGGCCTCC 540

0075055-0104

	AATTATGCAC	AGTACCGGGT	TGCCC GCGCT	ACTATCCGTT	ACCGGCCCCCT	AGTGCCTAAT	600
	GCAGTTGGAG	GCTATGCTAT	ATCCATTTCT	TTCTGGCCTC	AAACAACCAC	AACCCCTACA	660
5	TCTGTTGACA	TGAATTCCAT	TACTTCCACT	GATGTCAGGA	TTCTTGTTCA	ACCTGGCATA	720
	GCATCTGAAT	TGGTCATCCC	AAGCGAGCGC	CTTCACTACC	GCAATCAAGG	TTGGCGCTCG	780
	GTTGAGACAT	CTGGTGTTGC	TGAGGAGGAA	GCCACCTCCG	GTCTTGTCAT	GTTATGCATA	840
10	CATGGCTCTC	CAGTTAACTC	CTATACCAAT	ACCCCTTATA	CCGGTGCCCT	TGGCTTACTG	900
	GACTTTGCCT	TAGAGCTTGA	GTTTCGCAAT	CTCACCACCT	GTAACACCAA	TACACGTGTG	960
15	TCCCGTTACT	CCAGCACGGC	CCGTCACCGG	CTCCGCCGAG	GGGCCGACGG	GACTIONGAG	1020
	CTGACCACAA	CTGCAGCCAC	CAGGTTTCATG	AAAGATCTCC	ACTTTACCGG	CCTTAATGGG	1080
	GTAGGTGAAG	TCGGCCGCGG	GATAGCTCTA	ACATTACTTA	ACCTTGCTGA	CACGCTCCTC	1140
20	GGCGGGCTCC	CGACAGAATT	AATTTGTCG	GCTGGCGGGC	AACTGTTTTA	TTCCCGCCCG	1200
	GTTGTCTCAG	CCAATGGCGA	GCCAACCGTG	AAGCTCTATA	CATCAGTGGA	GAATGCTCAG	1260
25	CAGGATAAGG	GTGTTGCTAT	CCCCCACGAT	ATCGATCTTG	GTGATTGCGG	TGTGGTCATT	1320
	CAGGATTATG	ACAACCAGCA	TGAGCAGGAT	CGGCCACCC	CGTCGCCTGC	GCCATCTCGG	1380
	CCTTTTTTCTG	TTCTCCGAGC	AAATGATGTA	CTTTGGCTGT	CCCTCACTGC	AGCCGAGTAT	1440
30	GACCAGTCCA	CTTACGGGTC	GTCAACTGGC	CCGGTTTATA	TCTCGGACAG	CGTGACTTTG	1500
	GTGAATGTTG	CGACTGGCGC	GCAGGCCGTA	GCCCCGATCGC	TTGACTGGTC	CAAAGTCACC	1560
35	CTCGACGGGC	GGCCCCCTCCC	GACTGTTGAG	CAATATTCCA	AGACATTCTT	TGTGCTCCCC	1620
	CTTCGTGGCA	AGCTCTCCTT	TTGGGAGGCC	GGCACAACAA	AAGCAGGTTA	TCCTTATAAT	1680
	TATAATACTA	CTGCTAGTGA	CCAGATTCTG	ATTGAAAATG	CTGCCGGCCA	TCGGGTCGCC	1740
40	ATTTCAACCT	ATACCACCAG	GCTTGGGGCC	GGTCCGGTCG	CCATTTCTGC	GGCCGCGGTT	1800

TTGGCTCCAC GCTCCGCCCT GGCTCTGCTG GAGGATACTT TTGATTATCC GGGGCGGGCG 1860  
CACACATTTG ATGACTTCTG CCCTGAATGC CGCGCTTTAG GCCTCCAGGG TTGTGCTTTC 1920  
5 CAGTCAACTG TCGCTGAGCT CCAGCGCCTT AAAGTTAAGG TGGGTAAAAC TCGGGAGTTG 1980  
TAGTTTATTT GGCTGTGCCC ACCTACTTAT ATCTGCTGAT TTCCTTTATT TCCTTTTTCT 2040  
CGGTCCCGCG CTCCCTGA 2058

10

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 1647 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

20

## (iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

25

- (C) INDIVIDUAL ISOLATE: Hepatitis E virus (Burma) r62kDa,  
FIGURE 2

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

30

GCGGTCGCTC CGGCCCATGA CACCCCGCCA GTGCCTGATG TCGACTCCCG CGGCGCCATC 60  
TTGCGCCGGC AGTATAACCT ATCAACATCT CCCCTTACCT CTTCCGTGGC CACCGGCACT 120  
AACCTGGTTC TTTATGCCGC CCCTCTTAGT CCGCTTTTAC CCCTTCAGGA CGGCACCAAT 180  
35 ACCCATATAA TGGCCACGGA AGCTTCTAAT TATGCCCAGT ACCGGGTTGC CCGTGCCACA 240  
ATCCGTTACC GCCCGCTGGT CCCCAATGCT GTCGGCGGTT ACGCCATCTC CATCTCATTC 300  
40 TGGCCACAGA CCACCACCAC CCCGACGTCC GTTGATATGA ATTCAATAAC CTCGACGGAT 360

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	GTTCGTATTT TAGTCCAGCC CGGCATAGCC TCTGAGCTTG TGATCCCAAG TGAGCGCCTA	420
	CACTATCGTA ACCAAGGCTG GCGCTCCGTC GAGACCTCTG GGGTGGCTGA GGAGGAGGCT	480
5	ACCTCTGGTC TTGTTATGCT TTGCATACAT GGCTCACTCG TAAATTCCTA TACTAATACA	540
	CCCTATACCG GTGCCCTCGG GCTGTTGGAC TTTGCCCTTG AGCTTGAGTT TCGCAACCTT	600
10	ACCCCCGGTA ACACCAATAC GCGGGTCTCC CGTTATTCCA GCACTGCTCG CCACCGCCTT	660
	CGTCGCGGTG CGGACGGGAC TGCCGAGCTC ACCACCACGG CTGCTACCCG CTTTATGAAG	720
	GACCTCTATT TTACTAGTAC TAATGGTGTC GGTGAGATCG GCCGCGGGAT AGCCCTCACC	780
15	CTGTTCAACC TTGCTGACAC TCTGCTTGGC GGCCTGCCGA CAGAATTGAT TTCGTCGGCT	840
	GGTGGCCAGC TGTTCTACTC CCGTCCCGTT GTCTCAGCCA ATGGCGAGCC GACTGTTAAG	900
20	TTGTATACAT CTGTAGAGAA TGCTCAGCAG GATAAGGGTA TTGCAATCCC GCATGACATT	960
	GACCTCGGAG AATCTCGTGT GGTTATTCAG GATTATGATA ACCAACATGA ACAAGATCGG	1020
	CCGACGCCTT CTCCAGCCCC ATCGCGCCCT TTCTCTGTCC TTCGAGCTAA TGATGTGCTT	1080
25	TGGCTCTCTC TCACCGCTGC CGAGTATGAC CAGTCCACTT ATGGCTCTTC GACTGGCCCA	1140
	GTTTATGTTT CTGACTCTGT GACCTTGGTT AATGTTGCGA CCGGCGCGCA GGCCGTTGCC	1200
30	CGGTCGCTCG ATTGGACCAA GGTCACACTT GACGGTCGCC CCCTCTCCAC CATCCAGCAG	1260
	TACTCGAAGA CCTTCTTTGT CCTGCCGCTC CGCGGTAAGC TCTCTTTCTG GGAGGCAGGC	1320
	ACAACTAAAG CCGGGTACCC TTATAATTAT AACACCACTG CTAGCGACCA ACTGCTTGTC	1380
35	GAGAATGCCG CCGGGCACCG GGTGCTATT TCCACTTACA CCACTAGCCT GGGTGCTGGT	1440
	CCCGTCTCCA TTTCTGCGGT TGCCGTTTGA GCCCCCACT CTGCGCTAGC ATTGCTTGAG	1500
40	GATACCTTGG ACTACCCTGC CCGCGCCCAT ACTTTTGATG ATTTCTGCCC AGAGTGCCGC	1560
	CCCCTTGGCC TTCAGGGCTG CGCTTTCCAG TCTACTGTCG CTGAGCTTCA GCGCCTTAAG	1620

108-99999999

ATGAAGGTGG GTAAACTCG GGAGTTG

1647

## (2) INFORMATION FOR SEQ ID NO:4:

5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1647 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

15 (vi) ORIGINAL SOURCE:  
 (C) INDIVIDUAL ISOLATE: Hepatitis E virus (Mexico strain)  
 r62kDa, FIGURE 2

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCTGTGGCGC	CTGCCCATGA	CACCTCACCC	GTCCCGGACG	TTGATTCTCG	CGGTGCAATT	60
CTACGCCGCC	AGTATAATTT	GTCTACTTCA	CCCCTGACAT	CCTCTGTGGC	CTCTGGCACT	120
AATTTAGTCC	TGTATGCAGC	CCCCCTTAAT	CCGCCTCTGC	CGCTGCAGGA	CGGTACTAAT	180
ACTCACATTA	TGGCCACAGA	GGCCTCCAAT	TATGCACAGT	ACCGGGTTGC	CCGCGCTACT	240
ATCCGTTACC	GGCCCCTAGT	GCCTAATGCA	GTTGGAGGCT	ATGCTATATC	CATTTCTTTC	300
TGGCCTCAAA	CAACCACAAC	CCCTACATCT	GTTGACATGA	ATTCCATTAC	TTCCACTGAT	360
GTCAGGATTC	TTGTTCAACC	TGGCATAGCA	TCTGAATTGG	TCATCCCAAG	CGAGCGCCTT	420
CACTACCGCA	ATCAAGGTTG	GCGCTCGGTT	GAGACATCTG	GTGTTGCTGA	GGAGGAAGCC	480
ACCTCCGGTC	TTGTCATGTT	ATGCATACAT	GGCTCTCCAG	TTAACTCCTA	TACCAATACC	540
CCTTATACCG	GTGCCCTTGG	CTTACTGGAC	TTTGCCTTAG	AGCTTGAGTT	TCGCAATCTC	600
ACCACCTGTA	ACACCAATAC	ACGTGTGTCC	CGTTACTCCA	GCACGGCCCCG	TCACCGGCTC	660



CGCCGAGGGG CCGACGGGAC TCGGAGCTG ACCACAACCTG CAGCCACCAG GTTCATGAAA 720  
GATCTCCACT TTACCGGCCT TAATGGGGTA GGTGAAGTCG GCCGCGGGAT AGCTCTAACA 780  
5 TTACTIONAACC TTGCTGACAC GCTCCTCGGC GGGCTCCCGA CAGAATTAAT TTCGTCGGCT 840  
GGCGGGCAAC TGTTTTATTG CCGCCCGGTT GTCTCAGCCA ATGGCGAGCC AACCGTGAAG 900  
CTCTATACAT CAGTGGAGAA TGCTCAGCAG GATAAGGGTG TTGCTATCCC CCACGATATC 960  
10 GATCTTGGTG ATTCGCGTGT GGTGATTGAG GATTATGACA ACCAGCATGA GCAGGATCGG 1020  
CCCACCCCGT CGCCTGCGCC ATCTCGGCCT TTTTCTGTTC TCCGAGCAAA TGATGTACTT 1080  
15 TGGCTGTCCC TCACTGCAGC CGAGTATGAC CAGTCCACTT ACGGGTCGTC AACTGGCCCCG 1140  
GTTTATATCT CGGACAGCGT GACTTTGGTG AATGTTGCGA CTGGCGCGCA GGCCGTAGCC 1200  
CGATCGCTTG ACTGGTCCAA AGTCACCCTC GACGGGCGGC CCCTCCCGAC TGTTGAGCAA 1260  
20 TATTCCAAGA CATTCTTTGT GCTCCCCCTT CGTGGCAAGC TCTCCTTTTG GGAGGCCGGC 1320  
ACAACAAAAG CAGGTTATCC TTATAATTAT AATACTACTG CTAGTGACCA GATTCTGATT 1380  
25 GAAAATGCTG CCGGCCATCG GGTCGCCATT TCAACCTATA CCACCAGGCT TGGGGCCGGT 1440  
CCGGTCGCCA TTTCTGCGGC CGCGGTTTTG GCTCCACGCT CCGCCCTGGC TCTGCTGGAG 1500  
GATACTTTTG ATTATCCGGG GCGGGCGCAC ACATTTGATG ACTTCTGCCC TGAATGCCGC 1560  
30 GCTTTAGGCC TCCAGGGTTG TGCTTTCCAG TCAACTGTCTG CTGAGCTCCA GCGCCTTAAA 1620  
GTTAAGGTGG GTAAAACTCG GGAGTTG 1647  
35 (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 984 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

5 (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain) SG3  
region

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGTGCGGACG GGACTGCCGA GCTCACCACC ACGGCTGCTA CCCGCTTTAT GAAGGACCTC 60  
TATTTTACTA GTACTAATGG TGTGGTGAG ATCGGCCGCG GGATAGCCCT CACCCTGTTC 120  
15 AACCTTGCTG AACTCTGCT TGGCGGCCTG CCGACAGAAT TGATTTTCGTC GGCTGGTGGC 180  
CAGCTGTTCT ACTCCCGTCC CGTTGTCTCA GCCAATGGCG AGCCGACTGT TAAGTTGTAT 240  
20 ACATCTGTAG AGAATGCTCA GCAGGATAAG GGTATTGCAA TCCCGCATGA CATTGACCTC 300  
GGAGAATCTC GTGTGGTTAT TCAGGATTAT GATAACCAAC ATGAACAAGA TCGGCCGACG 360  
CCTTCTCCAG CCCCATCGCG CCCTTTCTCT GTCCTTCGAG CTAATGATGT GCTTTGGCTC 420  
25 TCTCTCACCG CTGCCGAGTA TGACCAGTCC ACTTATGGCT CTTGCGACTGG CCCAGTTTAT 480  
GTTTCTGACT CTGTGACCTT GGTTAATGTT GCGACCGGCG CGCAGGCCGT TGCCCGGTCG 540  
30 CTCGATTGGA CCAAGGTCAC ACTTGACGGT CGCCCCCTCT CCACCATCCA GCAGTACTCG 600  
AAGACCTTCT TTGTCCTGCC GCTCCGCGGT AAGCTCTCTT TCTGGGAGGC AGGCACAAC 660  
AAAGCCGGGT ACCCTTATAA TTATAACACC ACTGCTAGCG ACCAACTGCT TGTCGAGAAT 720  
35 GCCGCCGGGC ACCGGGTCGC TATTTCCACT TACACCACTA GCCTGGGTGC TGGTCCCGTC 780  
TCCATTTCTG CGGTTGCCGT TTTAGCCCC CACTCTGCGC TAGCATTGCT TGAGGATACC 840  
40 TTGGACTACC CTGCCGCGC CCATACTTTT GATGATTCTT GCCCAGAGTG CCGCCCCCTT 900

5 (2) INFORMATION FOR SEQ ID NO:6:

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ATCTCGGACA GCGTGACTTT GGTGAATGTT GCGACTGGCG CGCAGGCCGT AGCCCGATCG 540

CTTGACTGGT CCAAAGTCAC CCTCGACGGG CGGCCCTCC CGACTGTTGA GCAATATTCC 600

AAGACATTCT TTGTGCTCCC CCTTCGTGGC AAGCTCTCCT TTTGGGAGGC CGGCACAACA 660

5 AAAGCAGGTT ATCCTTATAA TTATAATACT ACTGCTAGTG ACCAGATTCT GATTGAAAAT 720

GCTGCCGGCC ATCGGGTCGC CATTTCACC TATACCACCA GGCTTGGGGC CGGTCCGGTC 780

10 GCCATTTCTG CGGCCGCGGT TTTGGCTCCA CGCTCCGCCC TGGCTCTGCT GGAGGATACT 840

TTTGATTATC CGGGGCGGGC GCACACATT GATGACTTCT GCCCTGAATG CCGCGCTTTA 900

GGCCTCCAGG GTTGTGCTTT CCAGTCAACT GTCGCTGAGC TCCAGCGCCT TAAAGTTAAG 960

15 GTGGGTAAAA CTCGGGAGTT GTAG 984

## (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 147 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

30 (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain)

406.3-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

35 ACCTTGACT ACCCTGCCCC CGCCATACT TTTGATGATT TCTGCCAGA GTGCCGCCCC 60

CTTGGCCTTC AGGGCTGCGC TTTCCAGTCT ACTGTCGCTG AGCTTCAGCG CCTTAAGATG 120

40 AAGGTGGGTA AACTCGGGA GTTGTAG 147

F0140-930940

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:		
20	ACTTTTGATT ATCCGGGGCG GCGCACACA TTTGATGACT TCTGCCCTGA ATGCCGCGCT	60
	TTAGGCCTCC AGGGTTGTGC TTTCCAGTCA ACTGTCGCTG AGCTCCAGCG CCTTAAAGTT	120
	AAGGTGGGTA AAACTCGGGA GTTGTAG	147

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 372 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:  
(C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma Strain)  
40 ORF-3 region

	ATGAATAACA	TGTCCTTTTGC	TGCGCCCATG	GGTTCGCGAC	CATGCGCCCT	CGGCCTATTT	60
5	TGTTGCTGCT	CCTCATGTTT	TTGCCTATGC	TGCCCCGCGC	ACCGCCCGGT	CAGCCGTCTG	120
	GCCGCCGTCG	TGGGCGGCGC	AGCGGCGGTT	CCGGCGGTGG	TTTCTGGGGT	GACCGGGTTG	180
10	ATTCTCAGCC	CTTCGCAATC	CCCTATATTC	ATCCAACCAA	CCCCTTCGCC	CCCGATGTCA	240
	CCGCTGCGGC	CGGGGCTGGA	CCTCGTGTTT	GCCAACCCGC	CCGACCACTC	GGCTCCGCTT	300
	GGCGTGACCA	GGCCCAGCGC	CCCGCCGTTG	CCTCACGTCG	TAGACCTACC	ACAGCTGGGG	360
15	CCGCGCCGCT	AA					372

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

30 (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico Strain)  
ORF-3 region

	ATGAATAACA TGTGGTTTGC TGC GCCCATG GGTTCGCCAC CATGCGCCCT AGGCCTCTTT	60
	TGCTGTTGTT CCTCTTGTTT CTGCCTATGT TGCCCGCGCC ACCGACCGGT CAGCCGTCTG	120
40	GCCGCCGTCG TGGGCGGCGC AGCGGCGGTA CCGGCGGTGG TTTCTGGGGT GACCGGGTTG	180

ATTCTCAGCC CTTCGCAATC CCCTATATTC ATCCAACCAA CCCCTTTGCC CCAGACGTTG 240  
 CCGCTGCGTC CGGGTCTGGA CCTCGCCTTC GCCAACCAGC CCGGCCACTT GGCTCCACTT 300  
 5 GGCGAGATCA GGCCCAGCGC CCCTCCGCTG CCTCCCGTCG CCGACCTGCC ACAGCCGGGG 360  
 CTGCGGCGCT GA 372

(2) INFORMATION FOR SEQ ID NO:11:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

20

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain)  
 406.4-2 region

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCCAACCCGC CCGACCACTC GGCTCCGCTT GGC GTGACCA GGCCCAGCGC CCCGCCGTTG 60  
 30 CCTCACGTCG TAGACCTACC ACAGCTGGGG CCGCGCCGC 99

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 99 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: DNA (genomic)

T01110-9909260

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico strain)  
406.4-2 region

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

10 GCCAACCAGC CCGGCCACTT GGCTCCACTT GGCGAGATCA GGCCCAGCGC CCCTCCGCTG 60  
CCTCCCCTCG CCGACCTGCC ACAGCCGGGG CTGCGGGCGC 99

(2) INFORMATION FOR SEQ ID NO:13:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 660 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

25

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain)  
ORF-2

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Arg Pro Arg Pro Ile Leu Leu Leu Leu Met Phe Leu Pro Met  
1 5 10 15

35

Leu Pro Ala Pro Pro Pro Gly Gln Pro Ser Gly Arg Arg Arg Gly Arg  
20 25 30

Arg Ser Gly Gly Ser Gly Gly Gly Phe Trp Gly Asp Arg Val Asp Ser  
35 40 45

40

Gln Pro Phe Ala Ile Pro Tyr Ile His Pro Thr Asn Pro Phe Ala Pro

00369066-0434  
F012F0-9909200



	50		55		60
	Asp Val Thr Ala Ala Ala Gly Ala Gly Pro Arg Val Arg Gln Pro Ala				
	65		70		75 80
5	Arg Pro Leu Gly Ser Ala Trp Arg Asp Gln Ala Gln Arg Pro Ala Val				
		85		90	95
	Ala Ser Arg Arg Arg Pro Thr Thr Ala Gly Ala Ala Pro Leu Thr Ala				
10		100		105	110
	Val Ala Pro Ala His Asp Thr Pro Pro Val Pro Asp Val Asp Ser Arg				
		115		120	125
15	Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro Leu Thr				
		130		135	140
	Ser Ser Val Ala Thr Gly Thr Asn Leu Val Leu Tyr Ala Ala Pro Leu				
	145		150		155 160
20	Ser Pro Leu Leu Pro Leu Gln Asp Gly Thr Asn Thr His Ile Met Ala				
		165		170	175
	Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Ala Arg Ala Thr Ile				
25		180		185	190
	Arg Tyr Arg Pro Leu Val Pro Asn Ala Val Gly Gly Tyr Ala Ile Ser				
		195		200	205
30	Ile Ser Phe Trp Pro Gln Thr Thr Thr Thr Pro Thr Ser Val Asp Met				
		210		215	220
	Asn Ser Ile Thr Ser Thr Asp Val Arg Ile Leu Val Gln Pro Gly Ile				
	225		230		235 240
35	Ala Ser Glu Leu Val Ile Pro Ser Glu Arg Leu His Tyr Arg Asn Gln				
		245		250	255
	Gly Trp Arg Ser Val Glu Thr Ser Gly Val Ala Glu Glu Glu Ala Thr				
40		260		265	270

009006-0104  
009006-0104

[illegible]

	Ser	Leu	Asp	Trp	Thr	Lys	Val	Thr	Leu	Asp	Gly	Arg	Pro	Leu	Ser	Thr
5			515					520					525			

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10      Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr Asn
       545                      550                      555                      560

```

15 His Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly Ala Gly Pro  
580 585 590

20	595	600	605												
Leu	Leu	Glu	Asp	Thr	Leu	Asp	Tyr	Pro	Ala	Arg	Ala	His	Thr	Phe	Asp
	610					615						620			

25            Asp Phe Cys Pro Glu Cys Arg Pro Leu Gly Leu Gln Gly Cys Ala Phe  
625                          630                          635                          640

30 Thr Arg Glu Leu  
660

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 660 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

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Asn Pro Pro Leu Pro Leu Gln Asp Gly Thr Asn Thr His Ile Met Ala  
165 170 175

Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Ala Arg Ala Thr Ile  
 180 185 190

5 Arg Tyr Arg Pro Leu Val Pro Asn Ala Val Gly Gly Tyr Ala Ile Ser  
 195 200 205

Ile Ser Phe Trp Pro Gln Thr Thr Thr Thr Pro Thr Ser Val Asp Met  
 210 215 220

10 Asn Ser Ile Thr Ser Thr Asp Val Arg Ile Leu Val Gln Pro Gly Ile  
 225 230 235 240

Ala Ser Glu Leu Val Ile Pro Ser Glu Arg Leu His Tyr Arg Asn Gln  
 245 250 255

15 Gly Trp Arg Ser Val Glu Thr Ser Gly Val Ala Glu Glu Glu Ala Thr  
 260 265 270

20 Ser Gly Leu Val Met Leu Cys Ile His Gly Ser Pro Val Asn Ser Tyr  
 275 280 285

Thr Asn Thr Pro Tyr Thr Gly Ala Leu Gly Leu Leu Asp Phe Ala Leu  
 290 295 300

25 Glu Leu Glu Phe Arg Asn Leu Thr Thr Cys Asn Thr Asn Thr Arg Val  
 305 310 315 320

Ser Arg Tyr Ser Ser Thr Ala Arg His Arg Leu Arg Arg Gly Ala Asp  
 325 330 335

30 Gly Thr Ala Glu Leu Thr Thr Thr Ala Ala Thr Arg Phe Met Lys Asp  
 340 345 350

35 Leu His Phe Thr Gly Leu Asn Gly Val Gly Glu Val Gly Arg Gly Ile  
 355 360 365

Ala Leu Thr Leu Leu Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu Pro  
 370 375 380

40 Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg Pro  
 385 390 395 400

0025006-01244

	Val	Val	Ser	Ala	Asn	Gly	Glu	Pro	Thr	Val	Lys	Leu	Tyr	Thr	Ser	Val
					405					410						415
5	Glu	Asn	Ala	Gln	Gln	Asp	Lys	Gly	Val	Ala	Ile	Pro	His	Asp	Ile	Asp
				420					425					430		
	Leu	Gly	Asp	Ser	Arg	Val	Val	Ile	Gln	Asp	Tyr	Asp	Asn	Gln	His	Glu
			435					440					445			
10	Gln	Asp	Arg	Pro	Thr	Pro	Ser	Pro	Ala	Pro	Ser	Arg	Pro	Phe	Ser	Val
		450					455					460				
	Leu	Arg	Ala	Asn	Asp	Val	Leu	Trp	Leu	Ser	Leu	Thr	Ala	Ala	Glu	Tyr
15	465					470					475					480
	Asp	Gln	Ser	Thr	Tyr	Gly	Ser	Ser	Thr	Gly	Pro	Val	Tyr	Ile	Ser	Asp
					485					490					495	
20	Ser	Val	Thr	Leu	Val	Asn	Val	Ala	Thr	Gly	Ala	Gln	Ala	Val	Ala	Arg
				500					505					510		
	Ser	Leu	Asp	Trp	Ser	Lys	Val	Thr	Leu	Asp	Gly	Arg	Pro	Leu	Pro	Thr
			515					520					525			
25	Val	Glu	Gln	Tyr	Ser	Lys	Thr	Phe	Phe	Val	Leu	Pro	Leu	Arg	Gly	Lys
		530					535					540				
	Leu	Ser	Phe	Trp	Glu	Ala	Gly	Thr	Thr	Lys	Ala	Gly	Tyr	Pro	Tyr	Asn
30	545					550					555					560
	Tyr	Asn	Thr	Thr	Ala	Ser	Asp	Gln	Ile	Leu	Ile	Glu	Asn	Ala	Ala	Gly
					565					570					575	
35	His	Arg	Val	Ala	Ile	Ser	Thr	Tyr	Thr	Thr	Arg	Leu	Gly	Ala	Gly	Pro
				580					585					590		
	Val	Ala	Ile	Ser	Ala	Ala	Ala	Val	Leu	Ala	Pro	Arg	Ser	Ala	Leu	Ala
				595				600					605			
40	Leu	Leu	Glu	Asp	Thr	Phe	Asp	Tyr	Pro	Gly	Arg	Ala	His	Thr	Phe	Asp
			610					615					620			

Gln Ser Thr Val Ala Glu Leu Gln Arg Leu Lys Val Lys Val Gly Lys  
645 650 655

10 (2) INFORMATION FOR SEQ ID NO:15:

(A) LENGTH: 549 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Hepatitis E virus (Burma strain)  
r62kDa, FIGURE 4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ala Val Ala Pro Ala His Asp Thr Pro Pro Val Pro Asp Val Asp Ser  
1                   5                   10                   15

Arg Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro Leu  
20 25 30

Thr Ser Ser Val Ala Thr Gly Thr Asn Leu Val Leu Tyr Ala Ala Pro  
35 40 45

Leu Ser Pro Leu Leu Pro Leu Gln Asp Gly Thr Asn Thr His Ile Met  
50 55 60

Ala Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Ala Arg Ala Thr

	65					70						75					80
	Ile	Arg	Tyr	Arg	Pro	Leu	Val	Pro	Asn	Ala	Val	Gly	Gly	Tyr	Ala	Ile	
					85					90					95		
5																	
	Ser	Ile	Ser	Phe	Trp	Pro	Gln	Thr	Thr	Thr	Thr	Pro	Thr	Ser	Val	Asp	
				100					105					110			
10	Met	Asn	Ser	Ile	Thr	Ser	Thr	Asp	Val	Arg	Ile	Leu	Val	Gln	Pro	Gly	
			115					120						125			
	Ile	Ala	Ser	Glu	Leu	Val	Ile	Pro	Ser	Glu	Arg	Leu	His	Tyr	Arg	Asn	
		130					135					140					
15	Gln	Gly	Trp	Arg	Ser	Val	Glu	Thr	Ser	Gly	Val	Ala	Glu	Glu	Glu	Ala	
	145					150					155					160	
	Thr	Ser	Gly	Leu	Val	Met	Leu	Cys	Ile	His	Gly	Ser	Leu	Val	Asn	Ser	
				165						170					175		
20																	
	Tyr	Thr	Asn	Thr	Pro	Tyr	Thr	Gly	Ala	Leu	Gly	Leu	Leu	Asp	Phe	Ala	
			180						185					190			
	Leu	Glu	Leu	Glu	Phe	Arg	Asn	Leu	Thr	Pro	Gly	Asn	Thr	Asn	Thr	Arg	
25			195					200					205				
	Val	Ser	Arg	Tyr	Ser	Ser	Thr	Ala	Arg	His	Arg	Leu	Arg	Arg	Gly	Ala	
		210					215					220					
30	Asp	Gly	Thr	Ala	Glu	Leu	Thr	Thr	Thr	Ala	Ala	Thr	Arg	Phe	Met	Lys	
	225					230					235					240	
	Asp	Leu	Tyr	Phe	Thr	Ser	Thr	Asn	Gly	Val	Gly	Glu	Ile	Gly	Arg	Gly	
				245						250					255		
35																	
	Ile	Ala	Leu	Thr	Leu	Phe	Asn	Leu	Ala	Asp	Thr	Leu	Leu	Gly	Gly	Leu	
			260						265					270			
	Pro	Thr	Glu	Leu	Ile	Ser	Ser	Ala	Gly	Gly	Gln	Leu	Phe	Tyr	Ser	Arg	
40			275					280					285				



	Pro	Val	Val	Ser	Ala	Asn	Gly	Glu	Pro	Thr	Val	Lys	Leu	Tyr	Thr	Ser
	290						295					300				
5	Val	Glu	Asn	Ala	Gln	Gln	Asp	Lys	Gly	Ile	Ala	Ile	Pro	His	Asp	Ile
	305					310					315					320
	Asp	Leu	Gly	Glu	Ser	Arg	Val	Val	Ile	Gln	Asp	Tyr	Asp	Asn	Gln	His
					325					330					335	
10	Glu	Gln	Asp	Arg	Pro	Thr	Pro	Ser	Pro	Ala	Pro	Ser	Arg	Pro	Phe	Ser
				340					345					350		
	Val	Leu	Arg	Ala	Asn	Asp	Val	Leu	Trp	Leu	Ser	Leu	Thr	Ala	Ala	Glu
			355					360					365			
15	Tyr	Asp	Gln	Ser	Thr	Tyr	Gly	Ser	Ser	Thr	Gly	Pro	Val	Tyr	Val	Ser
		370					375					380				
	Asp	Ser	Val	Thr	Leu	Val	Asn	Val	Ala	Thr	Gly	Ala	Gln	Ala	Val	Ala
20	385					390					395					400
	Arg	Ser	Leu	Asp	Trp	Thr	Lys	Val	Thr	Leu	Asp	Gly	Arg	Pro	Leu	Ser
					405					410					415	
25	Thr	Ile	Gln	Gln	Tyr	Ser	Lys	Thr	Phe	Phe	Val	Leu	Pro	Leu	Arg	Gly
				420					425					430		
	Lys	Leu	Ser	Phe	Trp	Glu	Ala	Gly	Thr	Thr	Lys	Ala	Gly	Tyr	Pro	Tyr
			435					440					445			
30	Asn	Tyr	Asn	Thr	Thr	Ala	Ser	Asp	Gln	Leu	Leu	Val	Glu	Asn	Ala	Ala
	450						455					460				
	Gly	His	Arg	Val	Ala	Ile	Ser	Thr	Tyr	Thr	Thr	Ser	Leu	Gly	Ala	Gly
35	465					470					475					480
	Pro	Val	Ser	Ile	Ser	Ala	Val	Ala	Val	Leu	Ala	Pro	His	Ser	Ala	Leu
					485					490					495	
40	Ala	Leu	Leu	Glu	Asp	Thr	Leu	Asp	Tyr	Pro	Ala	Arg	Ala	His	Thr	Phe
				500					505					510		

Lys Thr Arg Glu Leu  
545

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (C) INDIVIDUAL ISOLATE: Hepatitis E virus (Mexico strain)  
r62kDa, FIGURE 4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

	Ala	Val	Ala	Pro	Ala	His	Asp	Thr	Ser	Pro	Val	Pro	Asp	Val	Asp	Ser
30	1				5					10					15	

Arg Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro Leu  
20 25 30

[illegible]

Leu Asn Pro Pro Leu Pro Leu Gln Asp Gly Thr Asn Thr His Ile Met  
50 55 60

40 Ala Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Ala Arg Ala Thr

	65					70						75					80
	Ile	Arg	Tyr	Arg	Pro	Leu	Val	Pro	Asn	Ala	Val	Gly	Gly	Tyr	Ala	Ile	
					85					90					95		
5																	
	Ser	Ile	Ser	Phe	Trp	Pro	Gln	Thr	Thr	Thr	Thr	Pro	Thr	Ser	Val	Asp	
				100					105					110			
10	Met	Asn	Ser	Ile	Thr	Ser	Thr	Asp	Val	Arg	Ile	Leu	Val	Gln	Pro	Gly	
			115					120						125			
	Ile	Ala	Ser	Glu	Leu	Val	Ile	Pro	Ser	Glu	Arg	Leu	His	Tyr	Arg	Asn	
		130					135						140				
15	Gln	Gly	Trp	Arg	Ser	Val	Glu	Thr	Ser	Gly	Val	Ala	Glu	Glu	Glu	Ala	
	145					150					155					160	
	Thr	Ser	Gly	Leu	Val	Met	Leu	Cys	Ile	His	Gly	Ser	Pro	Val	Asn	Ser	
				165						170					175		
20																	
	Tyr	Thr	Asn	Thr	Pro	Tyr	Thr	Gly	Ala	Leu	Gly	Leu	Leu	Asp	Phe	Ala	
			180						185					190			
	Leu	Glu	Leu	Glu	Phe	Arg	Asn	Leu	Thr	Thr	Cys	Asn	Thr	Asn	Thr	Arg	
25			195					200					205				
	Val	Ser	Arg	Tyr	Ser	Ser	Thr	Ala	Arg	His	Arg	Leu	Arg	Arg	Gly	Ala	
		210					215					220					
30	Asp	Gly	Thr	Ala	Glu	Leu	Thr	Thr	Thr	Ala	Ala	Thr	Arg	Phe	Met	Lys	
	225					230					235					240	
	Asp	Leu	His	Phe	Thr	Gly	Leu	Asn	Gly	Val	Gly	Glu	Val	Gly	Arg	Gly	
				245						250					255		
35																	
	Ile	Ala	Leu	Thr	Leu	Leu	Asn	Leu	Ala	Asp	Thr	Leu	Leu	Gly	Gly	Leu	
			260						265					270			
	Pro	Thr	Glu	Leu	Ile	Ser	Ser	Ala	Gly	Gly	Gln	Leu	Phe	Tyr	Ser	Arg	
40			275					280					285				

	Pro	Val	Val	Ser	Ala	Asn	Gly	Glu	Pro	Thr	Val	Lys	Leu	Tyr	Thr	Ser
	290						295					300				
5	Val	Glu	Asn	Ala	Gln	Gln	Asp	Lys	Gly	Val	Ala	Ile	Pro	His	Asp	Ile
	305				310						315					320
	Asp	Leu	Gly	Asp	Ser	Arg	Val	Val	Ile	Gln	Asp	Tyr	Asp	Asn	Gln	His
				325						330					335	
10	Glu	Gln	Asp	Arg	Pro	Thr	Pro	Ser	Pro	Ala	Pro	Ser	Arg	Pro	Phe	Ser
				340					345					350		
	Val	Leu	Arg	Ala	Asn	Asp	Val	Leu	Trp	Leu	Ser	Leu	Thr	Ala	Ala	Glu
		355						360					365			
15	Tyr	Asp	Gln	Ser	Thr	Tyr	Gly	Ser	Ser	Thr	Gly	Pro	Val	Tyr	Ile	Ser
	370						375					380				
	Asp	Ser	Val	Thr	Leu	Val	Asn	Val	Ala	Thr	Gly	Ala	Gln	Ala	Val	Ala
20	385				390						395					400
	Arg	Ser	Leu	Asp	Trp	Ser	Lys	Val	Thr	Leu	Asp	Gly	Arg	Pro	Leu	Pro
				405						410					415	
25	Thr	Val	Glu	Gln	Tyr	Ser	Lys	Thr	Phe	Phe	Val	Leu	Pro	Leu	Arg	Gly
			420						425					430		
	Lys	Leu	Ser	Phe	Trp	Glu	Ala	Gly	Thr	Thr	Lys	Ala	Gly	Tyr	Pro	Tyr
		435						440					445			
30	Asn	Tyr	Asn	Thr	Thr	Ala	Ser	Asp	Gln	Ile	Leu	Ile	Glu	Asn	Ala	Ala
	450						455					460				
	Gly	His	Arg	Val	Ala	Ile	Ser	Thr	Tyr	Thr	Thr	Arg	Leu	Gly	Ala	Gly
35	465				470						475					480
	Pro	Val	Ala	Ile	Ser	Ala	Ala	Ala	Val	Leu	Ala	Pro	Arg	Ser	Ala	Leu
				485						490					495	
40	Ala	Leu	Leu	Glu	Asp	Thr	Phe	Asp	Tyr	Pro	Gly	Arg	Ala	His	Thr	Phe
				500					505					510		

40 Ser Arg Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr  
65 70 75 80

	Thr	Ser	Val	Glu	Asn	Ala	Gln	Gln	Asp	Lys	Gly	Ile	Ala	Ile	Pro	His
					85					90					95	
5	Asp	Ile	Asp	Leu	Gly	Glu	Ser	Arg	Val	Val	Ile	Gln	Asp	Tyr	Asp	Asn
	100								105					110		
	Gln	His	Glu	Gln	Asp	Arg	Pro	Thr	Pro	Ser	Pro	Ala	Pro	Ser	Arg	Pro
	115				120				125							
10	Phe	Ser	Val	Leu	Arg	Ala	Asn	Asp	Val	Leu	Trp	Leu	Ser	Leu	Thr	Ala
	130				135				140							
	Ala	Glu	Tyr	Asp	Gln	Ser	Thr	Tyr	Gly	Ser	Ser	Thr	Gly	Pro	Val	Tyr
	145				150				155				160			
15	Val	Ser	Asp	Ser	Val	Thr	Leu	Val	Asn	Val	Ala	Thr	Gly	Ala	Gln	Ala
	165				170				175							
20	Val	Ala	Arg	Ser	Leu	Asp	Trp	Thr	Lys	Val	Thr	Leu	Asp	Gly	Arg	Pro
	180				185				190							
	Leu	Ser	Thr	Ile	Gln	Gln	Tyr	Ser	Lys	Thr	Phe	Phe	Val	Leu	Pro	Leu
	195				200				205							
25	Arg	Gly	Lys	Leu	Ser	Phe	Trp	Glu	Ala	Gly	Thr	Thr	Lys	Ala	Gly	Tyr
	210				215				220							
	Pro	Tyr	Asn	Tyr	Asn	Thr	Thr	Ala	Ser	Asp	Gln	Leu	Leu	Val	Glu	Asn
	225				230				235				240			
30	Ala	Ala	Gly	His	Arg	Val	Ala	Ile	Ser	Thr	Tyr	Thr	Thr	Ser	Leu	Gly
	245				250				255							
	Ala	Gly	Pro	Val	Ser	Ile	Ser	Ala	Val	Ala	Val	Leu	Ala	Pro	His	Ser
35	260				265				270							
	Ala	Leu	Ala	Leu	Leu	Glu	Asp	Thr	Leu	Asp	Tyr	Pro	Ala	Arg	Ala	His
	275				280				285							
40	Thr	Phe	Asp	Asp	Phe	Cys	Pro	Glu	Cys	Arg	Pro	Leu	Gly	Leu	Gln	Gly
	290				295				300							

Val Gly Lys Thr Arg Glu Leu  
325

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico strain)  
SG3 region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Gly Ala Asp Gly Thr Ala Glu Leu Thr Thr Thr Ala Ala Thr Arg Phe  
1                 5                 10                 15

Met Lys Asp Leu His Phe Thr Gly Leu Asn Gly Val Gly Glu Val Gly  
20 25 30

Arg Gly Ile Ala Leu Thr Leu Leu Asn Leu Ala Asp Thr Leu Leu Gly  
35 40 45

Gly Leu Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr  
50 55 60

Ser Arg Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr  
65 70 75 80

Thr Ser Val Glu Asn Ala Gln Gln Asp Lys Gly Val Ala Ile Pro His  
85 90 95

	Asp	Ile	Asp	Leu	Gly	Asp	Ser	Arg	Val	Val	Ile	Gln	Asp	Tyr	Asp	Asn	
				100					105							110	
5	Gln	His	Glu	Gln	Asp	Arg	Pro	Thr	Pro	Ser	Pro	Ala	Pro	Ser	Arg	Pro	
			115					120					125				
	Phe	Ser	Val	Leu	Arg	Ala	Asn	Asp	Val	Leu	Trp	Leu	Ser	Leu	Thr	Ala	
		130					135					140					
10	Ala	Glu	Tyr	Asp	Gln	Ser	Thr	Tyr	Gly	Ser	Ser	Thr	Gly	Pro	Val	Tyr	
	145					150					155					160	
	Ile	Ser	Asp	Ser	Val	Thr	Leu	Val	Asn	Val	Ala	Thr	Gly	Ala	Gln	Ala	
				165					170						175		
15	Val	Ala	Arg	Ser	Leu	Asp	Trp	Ser	Lys	Val	Thr	Leu	Asp	Gly	Arg	Pro	
			180						185					190			
	Leu	Pro	Thr	Val	Glu	Gln	Tyr	Ser	Lys	Thr	Phe	Phe	Val	Leu	Pro	Leu	
20			195					200					205				
	Arg	Gly	Lys	Leu	Ser	Phe	Trp	Glu	Ala	Gly	Thr	Thr	Lys	Ala	Gly	Tyr	
		210					215					220					
25	Pro	Tyr	Asn	Tyr	Asn	Thr	Thr	Ala	Ser	Asp	Gln	Ile	Leu	Ile	Glu	Asn	
	225					230					235					240	
	Ala	Ala	Gly	His	Arg	Val	Ala	Ile	Ser	Thr	Tyr	Thr	Thr	Arg	Leu	Gly	
				245						250					255		
30	Ala	Gly	Pro	Val	Ala	Ile	Ser	Ala	Ala	Ala	Val	Leu	Ala	Pro	Arg	Ser	
				260					265					270			
	Ala	Leu	Ala	Leu	Leu	Glu	Asp	Thr	Phe	Asp	Tyr	Pro	Gly	Arg	Ala	His	
35			275					280					285				
	Thr	Phe	Asp	Asp	Phe	Cys	Pro	Glu	Cys	Arg	Ala	Leu	Gly	Leu	Gln	Gly	
		290					295					300					
40	Cys	Ala	Phe	Gln	Ser	Thr	Val	Ala	Glu	Leu	Gln	Arg	Leu	Lys	Val	Lys	
	305					310					315					320	



Val Gly Lys Thr Arg Glu Leu  
325

(2) INFORMATION FOR SEQ ID NO:19:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

15

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain)  
406.4-2

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ala Asn Pro Pro Asp His Ser Ala Pro Leu Gly Val Thr Arg Pro Ser  
1 5 10 15

25

Ala Pro Pro Leu Pro His Val Val Asp Leu Pro Gln Leu Gly Pro Arg  
20 25 30

Arg

30

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 amino acids

35

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

40

(iii) HYPOTHETICAL: NO

0076966-0400

## (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico strain)  
406.4-2

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ala Asn Gln Pro Gly His Leu Ala Pro Leu Gly Glu Ile Arg Pro Ser  
1 5 10 15

10

Ala Pro Pro Leu Pro Pro Val Ala Asp Leu Pro Gln Pro Gly Leu Arg  
20 25 30

Arg

15

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 124 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

25

## (iii) HYPOTHETICAL: NO

## (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma Strain)  
ORF-3

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

35

Met Asn Asn Met Ser Phe Ala Ala Pro Met Gly Ser Arg Pro Cys Ala  
1 5 10 15

Leu Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys Pro  
20 25 30

40

Arg His Arg Pro Val Ser Arg Leu Ala Ala Val Val Gly Gly Ala Ala

35

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45

Ala Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser Pro  
50 55 60

5

Ser Gln Ser Pro Ile Phe Ile Gln Pro Thr Pro Ser Pro Pro Met Ser  
65 70 75 80

10

Pro Leu Arg Pro Gly Leu Asp Leu Val Phe Ala Asn Pro Pro Asp His  
85 90 95

Ser Ala Pro Leu Gly Val Thr Arg Pro Ser Ala Pro Pro Leu Pro His  
100 105 110

15

Val Val Asp Leu Pro Gln Leu Gly Pro Arg Arg Glx  
115 120

## (2) INFORMATION FOR SEQ ID NO:22:

20

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 124 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

30

- (vi) ORIGINAL SOURCE:  
(C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico Strain)  
ORF-3

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Asn Asn Met Trp Phe Ala Ala Pro Met Gly Ser Pro Pro Cys Ala  
1 5 10 15

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Leu Gly Leu Phe Cys Cys Cys Ser Ser Cys Phe Cys Leu Cys Cys Pro  
20 25 30

136-9365-1

Arg His Arg Pro Val Ser Arg Leu Ala Ala Val Val Gly Gly Ala Ala  
35 40 45

5 Ala Val Pro Ala Val Val Ser Gly Val Thr Gly Leu Ile Leu Ser Pro  
50 55 60

Ser Gln Ser Pro Ile Phe Ile Gln Pro Thr Pro Leu Pro Gln Thr Leu  
65 70 75 80

10 Pro Leu Arg Pro Gly Leu Asp Leu Ala Phe Ala Asn Gln Pro Gly His  
85 90 95

Leu Ala Pro Leu Gly Glu Ile Arg Pro Ser Ala Pro Pro Leu Pro Pro  
100 105 110

15 Val Ala Asp Leu Pro Gln Pro Gly Leu Arg Arg Glx  
115 120

(2) INFORMATION FOR SEQ ID NO:23:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 48 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

30 (vi) ORIGINAL SOURCE:  
(C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Burma strain)  
406.3-2

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Thr Leu Asp Tyr Pro Ala Arg Ala His Thr Phe Asp Asp Phe Cys Pro  
1 5 10 15

40 Glu Cys Arg Pro Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Val  
20 25 30

11610-3305260

5 (2) INFORMATION FOR SEQ ID NO:24:

10 (D) TOPOLOGY: linear

(B) TYPE: amino acid

(D) TOPOLOGY: linear

15

(iii) HYPOTHETICAL: NO

(C) INDIVIDUAL ISOLATE: Hepatitis E Virus (Mexico strain)  
406.3-2 region

25

Glu Cys Arg Ala Leu Gly Leu Gln Gly Cys Ala Phe Gln Ser Thr Val  
20 25 30

(2) INFORMATION FOR SEQ ID NO:25:

35 (A) LENGTH: 540 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

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Thr Ser Gly Leu Val Met Leu Cys Ile His Gly Ser Leu Val Asn Ser  
165 170 175

Tyr Thr Asn Thr Pro Tyr Thr Gly Ala Leu Gly Leu Leu Asp Phe Ala  
 180 185 190

5 Leu Glu Leu Glu Phe Arg Asn Leu Thr Pro Gly Asn Thr Asn Thr Arg  
 195 200 205

Val Ser Arg Tyr Ser Ser Thr Ala Arg His Arg Leu Arg Arg Gly Ala  
 210 215 220

10 Asp Gly Thr Ala Glu Leu Thr Thr Thr Ala Ala Thr Arg Phe Met Lys  
 225 230 235 240

Asp Leu Tyr Phe Thr Ser Thr Asn Gly Val Gly Glu Ile Gly Arg Gly  
 245 250 255

15 Ile Ala Leu Thr Leu Phe Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu  
 260 265 270

Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg  
 275 280 285

Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser  
 290 295 300

25 Val Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile  
 305 310 315 320

Asp Leu Gly Glu Ser Arg Val Val Ile Gln Asp Tyr Asp Asn Gln His  
 325 330 335

30 Glu Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser  
 340 345 350

Val Leu Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu  
 355 360 365

Tyr Asp Gln Ser Thr Tyr Gly Ser Ser Thr Gly Pro Val Tyr Val Ser  
 370 375 380

40 Asp Ser Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala  
 385 390 395 400

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	Thr	Ile	Gln	Gln	Tyr	Ser	Lys	Thr	Phe	Phe	Val	Leu	Pro	Leu	Arg	Gly
5				420					425					430		

10 Asn Tyr Asn Thr Thr Ala Ser Asp Gln Leu Leu Val Glu Asn Ala Ala  
450 455 460

15           Pro Val Ser Ile Ser Ala Val Ala Val Leu Ala Pro His Ser Ala Leu  
                            485                         490                         495

Asp Asp Phe Cys Pro Glu Cys Arg Pro Leu Gly Leu Gln Gly Cys Ala  
515 520 525

(2) INFORMATION FOR SEQ ID NO:26:

35 (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

40 (vi) ORIGINAL SOURCE:  
(C) INDIVIDUAL ISOLATE: Hepatitis E virus (Mexico strain)



r62kDa, 58.1 kDa

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

5 Ala Val Ala Pro Ala His Asp Thr Ser Pro Val Pro Asp Val Asp Ser  
1 5 10 15

Arg Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro Leu  
20 25 30

10 Thr Ser Ser Val Ala Ser Gly Thr Asn Leu Val Leu Tyr Ala Ala Pro  
35 40 45

Leu Asn Pro Pro Leu Pro Leu Gln Asp Gly Thr Asn Thr His Ile Met  
15 50 55 60

Ala Thr Glu Ala Ser Asn Tyr Ala Gln Tyr Arg Val Ala Arg Ala Thr  
65 70 75 80

20 Ile Arg Tyr Arg Pro Leu Val Pro Asn Ala Val Gly Gly Tyr Ala Ile  
85 90 95

Ser Ile Ser Phe Trp Pro Gln Thr Thr Thr Thr Pro Thr Ser Val Asp  
100 105 110

25 Met Asn Ser Ile Thr Ser Thr Asp Val Arg Ile Leu Val Gln Pro Gly  
115 120 125

Ile Ala Ser Glu Leu Val Ile Pro Ser Glu Arg Leu His Tyr Arg Asn  
30 130 135 140

Gln Gly Trp Arg Ser Val Glu Thr Ser Gly Val Ala Glu Glu Glu Ala  
145 150 155 160

35 Thr Ser Gly Leu Val Met Leu Cys Ile His Gly Ser Pro Val Asn Ser  
165 170 175

Tyr Thr Asn Thr Pro Tyr Thr Gly Ala Leu Gly Leu Leu Asp Phe Ala  
180 185 190

40 Leu Glu Leu Glu Phe Arg Asn Leu Thr Thr Cys Asn Thr Asn Thr Arg

P05969-1

195

200

205

5 Val Ser Arg Tyr Ser Ser Thr Ala Arg His Arg Leu Arg Arg Gly Ala  
210 215 220

Asp Gly Thr Ala Glu Leu Thr Thr Thr Ala Ala Thr Arg Phe Met Lys  
225 230 235 240

10 Asp Leu His Phe Thr Gly Leu Asn Gly Val Gly Glu Val Gly Arg Gly  
245 250 255

Ile Ala Leu Thr Leu Leu Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu  
260 265 270

15 Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg  
275 280 285

Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser  
290 295 300

20 Val Glu Asn Ala Gln Gln Asp Lys Gly Val Ala Ile Pro His Asp Ile  
305 310 315 320

25 Asp Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Asp Asn Gln His  
325 330 335

Glu Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser  
340 345 350

30 Val Leu Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu  
355 360 365

Tyr Asp Gln Ser Thr Tyr Gly Ser Ser Thr Gly Pro Val Tyr Ile Ser  
370 375 380

35 Asp Ser Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala  
385 390 395 400

40 Arg Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Pro  
405 410 415

101210-33003200

Thr Val Glu Gln Tyr Ser Lys Thr Phe Phe Val Leu Pro Leu Arg Gly  
420 425 430

5 Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr  
435 440 445

Asn Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala  
450 455 460

10 Gly His Arg Val Ala Ile Ser Thr Tyr Thr Thr Arg Leu Gly Ala Gly  
465 470 475 480

Pro Val Ala Ile Ser Ala Ala Ala Val Leu Ala Pro Arg Ser Ala Leu  
485 490 495

15 Ala Leu Leu Glu Asp Thr Phe Asp Tyr Pro Gly Arg Ala His Thr Phe  
500 505 510

20 Asp Asp Phe Cys Pro Glu Cys Arg Ala Leu Gly Leu Gln Gly Cys Ala  
515 520 525

Phe Gln Ser Thr Val Ala Glu Leu Gln Arg Leu Lys  
530 535 540

25 (2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 525 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35 (iii) HYPOTHETICAL: NO

(vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Hepatitis E virus (Burma strain)  
r62kDa, 56.5 kDa

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144-999999999

	Ala	Val	Ala	Pro	Ala	His	Asp	Thr	Pro	Pro	Val	Pro	Asp	Val	Asp	Ser	
	1					5				10						15	
5																	
	Arg	Gly	Ala	Ile	Leu	Arg	Arg	Gln	Tyr	Asn	Leu	Ser	Thr	Ser	Pro	Leu	
				20					25					30			
	Thr	Ser	Ser	Val	Ala	Thr	Gly	Thr	Asn	Leu	Val	Leu	Tyr	Ala	Ala	Pro	
10			35					40					45				
	Leu	Ser	Pro	Leu	Leu	Pro	Leu	Gln	Asp	Gly	Thr	Asn	Thr	His	Ile	Met	
		50					55					60					
15	Ala	Thr	Glu	Ala	Ser	Asn	Tyr	Ala	Gln	Tyr	Arg	Val	Ala	Arg	Ala	Thr	
	65					70					75					80	
	Ile	Arg	Tyr	Arg	Pro	Leu	Val	Pro	Asn	Ala	Val	Gly	Gly	Tyr	Ala	Ile	
					85					90					95		
20																	
	Ser	Ile	Ser	Phe	Trp	Pro	Gln	Thr	Thr	Thr	Thr	Pro	Thr	Ser	Val	Asp	
				100					105					110			
	Met	Asn	Ser	Ile	Thr	Ser	Thr	Asp	Val	Arg	Ile	Leu	Val	Gln	Pro	Gly	
25			115					120					125				
	Ile	Ala	Ser	Glu	Leu	Val	Ile	Pro	Ser	Glu	Arg	Leu	His	Tyr	Arg	Asn	
		130					135					140					
30	Gln	Gly	Trp	Arg	Ser	Val	Glu	Thr	Ser	Gly	Val	Ala	Glu	Glu	Glu	Ala	
	145					150					155					160	
	Thr	Ser	Gly	Leu	Val	Met	Leu	Cys	Ile	His	Gly	Ser	Leu	Val	Asn	Ser	
				165						170					175		
35																	
	Tyr	Thr	Asn	Thr	Pro	Tyr	Thr	Gly	Ala	Leu	Gly	Leu	Leu	Asp	Phe	Ala	
				180					185					190			
	Leu	Glu	Leu	Glu	Phe	Arg	Asn	Leu	Thr	Pro	Gly	Asn	Thr	Asn	Thr	Arg	
40			195					200					205				

	Val Ser Arg Tyr Ser Ser Thr Ala Arg His Arg Leu Arg Arg Gly Ala	
	210	215 220
5	Asp Gly Thr Ala Glu Leu Thr Thr Thr Ala Ala Thr Arg Phe Met Lys	
	225	230 235 240
	Asp Leu Tyr Phe Thr Ser Thr Asn Gly Val Gly Glu Ile Gly Arg Gly	
		245 250 255
10	Ile Ala Leu Thr Leu Phe Asn Leu Ala Asp Thr Leu Leu Gly Gly Leu	
		260 265 270
	Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg	
		275 280 285
15	Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser	
		290 295 300
	Val Glu Asn Ala Gln Gln Asp Lys Gly Ile Ala Ile Pro His Asp Ile	
20	305	310 315 320
	Asp Leu Gly Glu Ser Arg Val Val Ile Gln Asp Tyr Asp Asn Gln His	
		325 330 335
25	Glu Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser	
		340 345 350
	Val Leu Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu	
		355 360 365
30	Tyr Asp Gln Ser Thr Tyr Gly Ser Ser Thr Gly Pro Val Tyr Val Ser	
		370 375 380
	Asp Ser Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala	
35	385	390 395 400
	Arg Ser Leu Asp Trp Thr Lys Val Thr Leu Asp Gly Arg Pro Leu Ser	
		405 410 415
40	Thr Ile Gln Gln Tyr Ser Lys Thr Phe Phe Val Leu Pro Leu Arg Gly	
		420 425 430

1095996-0404  
FBI-DOJ-306560

Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr  
435 440 445

5 Asn Tyr Asn Thr Thr Ala Ser Asp Gln Leu Leu Val Glu Asn Ala Ala  
450 455 460

Gly His Arg Val Ala Ile Ser Thr Tyr Thr Thr Ser Leu Gly Ala Gly  
465 470 475 480

10 Pro Val Ser Ile Ser Ala Val Ala Val Leu Ala Pro His Ser Ala Leu  
485 490 495

Ala Leu Leu Glu Asp Thr Leu Asp Tyr Pro Ala Arg Ala His Thr Phe  
500 505 510

15 Asp Asp Phe Cys Pro Glu Cys Arg Pro Leu Gly Leu Gln  
515 520 525

(2) INFORMATION FOR SEQ ID NO:28:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 525 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

30 (vi) ORIGINAL SOURCE:

(C) INDIVIDUAL ISOLATE: Hepatitis E virus (Mexico strain)  
r62kDa, 56.5 kDa

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Ala Val Ala Pro Ala His Asp Thr Ser Pro Val Pro Asp Val Asp Ser  
1 5 10 15

40 Arg Gly Ala Ile Leu Arg Arg Gln Tyr Asn Leu Ser Thr Ser Pro Leu  
20 25 30

00769066-01404

	Thr	Ser	Ser	Val	Ala	Ser	Gly	Thr	Asn	Leu	Val	Leu	Tyr	Ala	Ala	Pro	
				35					40								45
5	Leu	Asn	Pro	Pro	Leu	Pro	Leu	Gln	Asp	Gly	Thr	Asn	Thr	His	Ile	Met	
		50					55					60					
	Ala	Thr	Glu	Ala	Ser	Asn	Tyr	Ala	Gln	Tyr	Arg	Val	Ala	Arg	Ala	Thr	
	65					70					75					80	
10	Ile	Arg	Tyr	Arg	Pro	Leu	Val	Pro	Asn	Ala	Val	Gly	Gly	Tyr	Ala	Ile	
					85					90					95		
	Ser	Ile	Ser	Phe	Trp	Pro	Gln	Thr	Thr	Thr	Thr	Pro	Thr	Ser	Val	Asp	
				100					105						110		
15	Met	Asn	Ser	Ile	Thr	Ser	Thr	Asp	Val	Arg	Ile	Leu	Val	Gln	Pro	Gly	
			115					120						125			
	Ile	Ala	Ser	Glu	Leu	Val	Ile	Pro	Ser	Glu	Arg	Leu	His	Tyr	Arg	Asn	
20		130					135					140					
	Gln	Gly	Trp	Arg	Ser	Val	Glu	Thr	Ser	Gly	Val	Ala	Glu	Glu	Glu	Ala	
	145					150					155					160	
25	Thr	Ser	Gly	Leu	Val	Met	Leu	Cys	Ile	His	Gly	Ser	Pro	Val	Asn	Ser	
				165						170					175		
	Tyr	Thr	Asn	Thr	Pro	Tyr	Thr	Gly	Ala	Leu	Gly	Leu	Leu	Asp	Phe	Ala	
				180					185					190			
30	Leu	Glu	Leu	Glu	Phe	Arg	Asn	Leu	Thr	Thr	Cys	Asn	Thr	Asn	Thr	Arg	
			195					200					205				
	Val	Ser	Arg	Tyr	Ser	Ser	Thr	Ala	Arg	His	Arg	Leu	Arg	Arg	Gly	Ala	
35		210					215					220					
	Asp	Gly	Thr	Ala	Glu	Leu	Thr	Thr	Thr	Ala	Ala	Thr	Arg	Phe	Met	Lys	
	225					230					235					240	
40	Asp	Leu	His	Phe	Thr	Gly	Leu	Asn	Gly	Val	Gly	Glu	Val	Gly	Arg	Gly	
						245				250						255	

5	Pro Thr Glu Leu Ile Ser Ser Ala Gly Gly Gln Leu Phe Tyr Ser Arg	275	280	285
	Pro Val Val Ser Ala Asn Gly Glu Pro Thr Val Lys Leu Tyr Thr Ser	290	295	300
10	Val Glu Asn Ala Gln Gln Asp Lys Gly Val Ala Ile Pro His Asp Ile	305	310	315
	Asp Leu Gly Asp Ser Arg Val Val Ile Gln Asp Tyr Asp Asn Gln His	325	330	335
15	Glu Gln Asp Arg Pro Thr Pro Ser Pro Ala Pro Ser Arg Pro Phe Ser	340	345	350
	Val Leu Arg Ala Asn Asp Val Leu Trp Leu Ser Leu Thr Ala Ala Glu	355	360	365
20	Tyr Asp Gln Ser Thr Tyr Gly Ser Ser Thr Gly Pro Val Tyr Ile Ser	370	375	380
	Asp Ser Val Thr Leu Val Asn Val Ala Thr Gly Ala Gln Ala Val Ala	385	390	395
25	Arg Ser Leu Asp Trp Ser Lys Val Thr Leu Asp Gly Arg Pro Leu Pro	405	410	415
30	Thr Val Glu Gln Tyr Ser Lys Thr Phe Phe Val Leu Pro Leu Arg Gly	420	425	430
	Lys Leu Ser Phe Trp Glu Ala Gly Thr Thr Lys Ala Gly Tyr Pro Tyr	435	440	445
35	Asn Tyr Asn Thr Thr Ala Ser Asp Gln Ile Leu Ile Glu Asn Ala Ala	450	455	460
	Gly His Arg Val Ala Ile Ser Thr Tyr Thr Thr Arg Leu Gly Ala Gly	465	470	475
40				480



Asp Asp Phe Cys Pro Glu Cys Arg Ala Leu Gly Leu Gln  
515 520 525

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(iii) HYPOTHETICAL: NO

(C) INDIVIDUAL ISOLATE: HEV 3' primer

ATTAGAAGCT TCCGTGGCCA TTATATG

27

(2) INFORMATION FOR SEQ ID NO:31:

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(iii) HYPOTHETICAL: YES

(v) FRAGMENT TYPE: internal

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(ix) FEATURE:

(ix) FEATURE:

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- (ix) FEATURE:

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- (ix) FEATURE:

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(ix) **FEATURE:**

- 25

(ix) **FEATURE:**

- 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

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Arg